

FIG. 1A

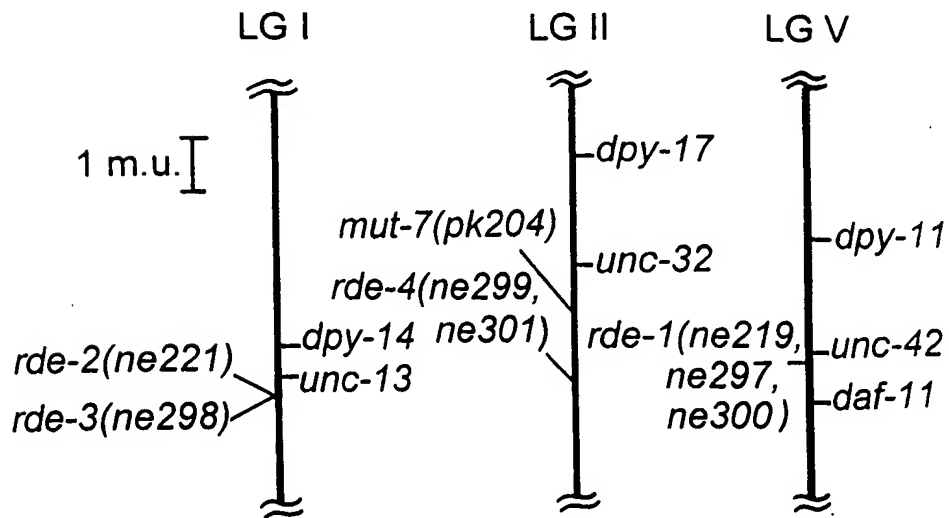
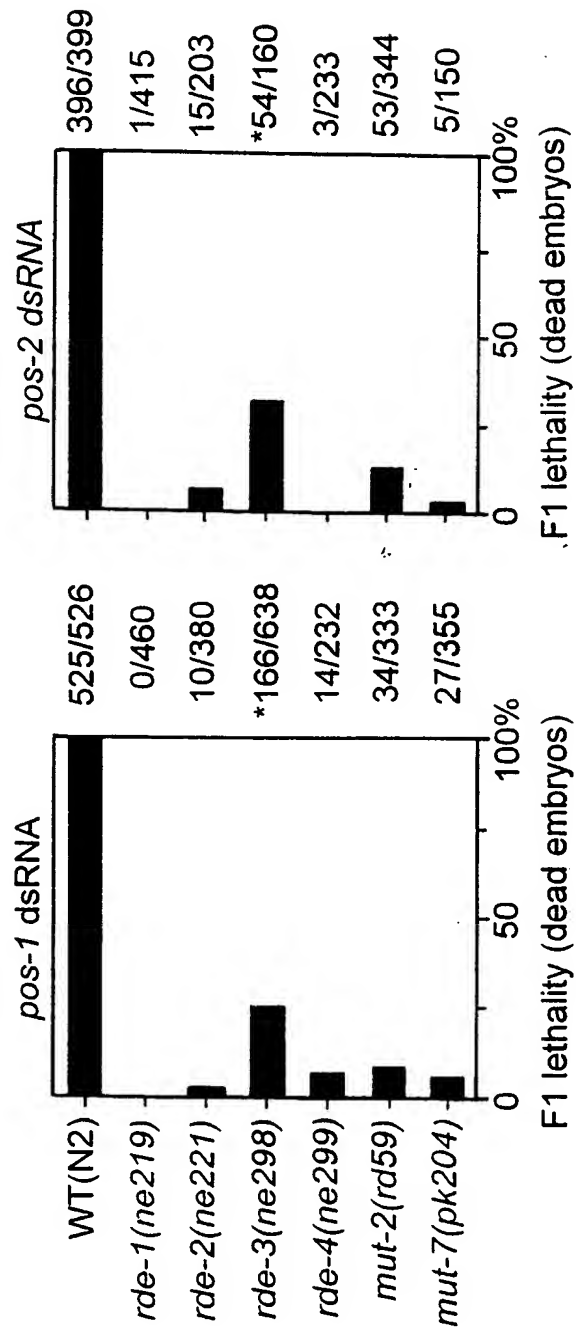
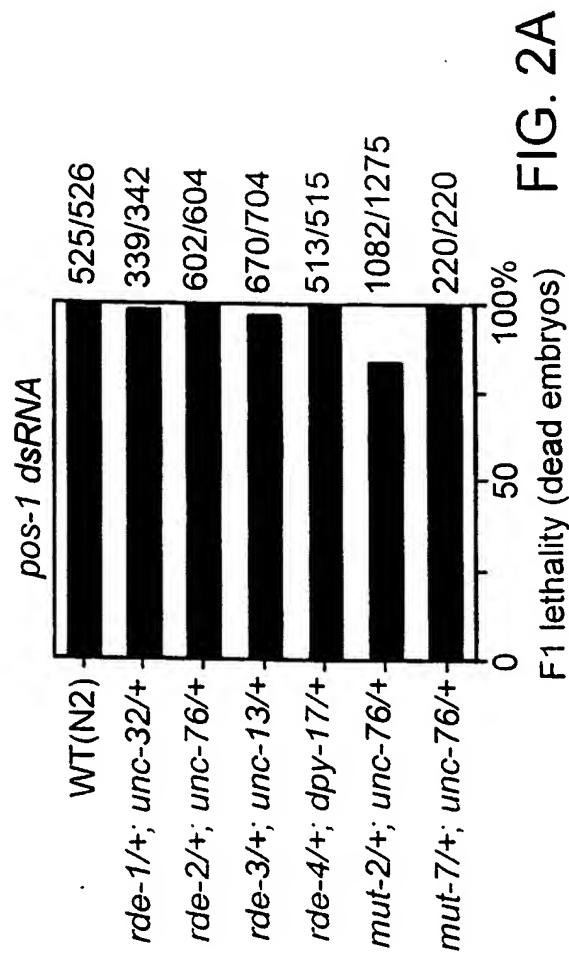


FIG. 1B



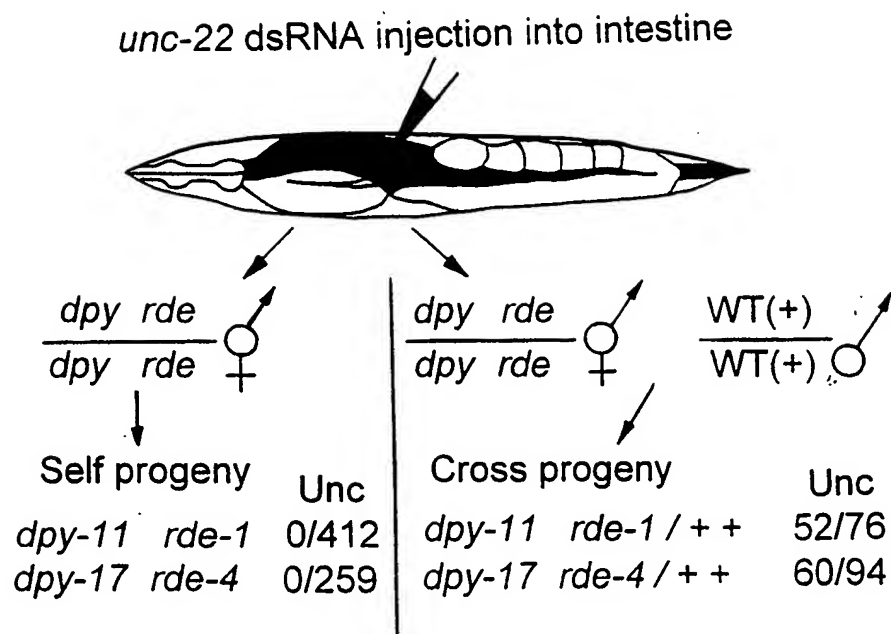


FIG. 3

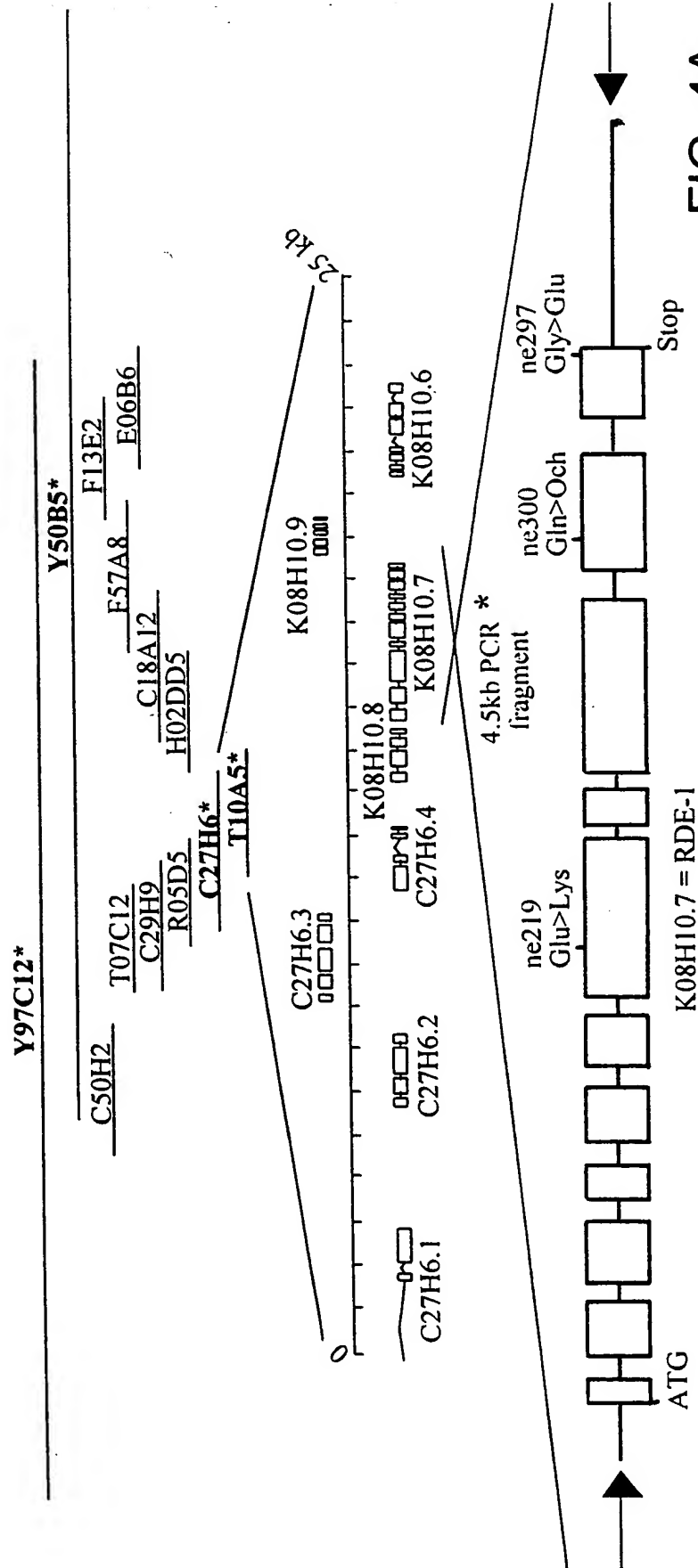


FIG. 4A

Title: RNA INTERFERENCE PATHWAY GENES AS TOOLS  
FOR TARGETED GENETIC INTERFERENCE

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RDE-1 203 VN-----EEIKVQAEAKNFVYDNNNSLRVPESFHDENRFEQSETEVAPRIEAWFGVIGIGIKELEDEGPVLN-----
F48F7.1 235 S-----AVRQFSVSLKVVQVSLSTLEDAVGRVROVPEAVQAVDVIER-HLPSEKRYTPVGRSEFFSPVPNAGVMAGSCPPQASGAV
eIF2C 77 -----GKDRIFKVSIGKVSCHVSOALHDAISGLPSVPEETIQALDVMR-HLPSEKRYTPVGRSEFTASEG-----CS
ZWILLE 226 GIINGPKRERSYKVAKEVARANMHHLGEFLAGKRADCEPRAVQIDETIER-ELSVAFECVGRSEFSSDIIK-----
Sting 189 -----RAGENIEIKKAVSVQSTDAEQFOVENLIRAMEGDLKMSRYDYDQAKIN-----

RDE-1 267 -----FAIVDKFYNAPKRGSLDYLIIIVDPQSONDDVRQDKTKKLMAGKMTIRQAARPRIR-----OLLENLRLKCAE
F48F7.1 319 AGGAHSAGQYHAESKIGGGRENVHGFHQSVRPSQWKMGINIDVSAIATYRSMPIETIAEVIELPQALAEERRALSDAQRVKFTKEIRGL
eIF2C 144 -----NE--LGGGREVWEGFHQSVRPSLMQMINIDVSATATYKAPVIEFVCEVDDFKSIEEQQN-PIEDQVRVKFTKEIRGL
ZWILLE 297 -----TEQRLGEGLESWCGEYQSSIRPTQMGISINIDMASAAFIETPVIETFAQLIGKDVLSKPLS---DSDAVKIKKGLRGV
Sting 244 -----LENERMQWPGYQTSIROHENDILICSEICHKVMETETLYNILSDAIRSDDYQSTFK-----R-AV

RDE-1 336 VWDNEMSRITERHLTFDLCEENSLVYKVTGKSD--RGRNAKTYDTTLFKIYEENKKFIEFPHLPPLVKVKGSKAREYAVPMEHLEVEHKPQ
F48F7.1 409 KIEITHCGGOMRRKRYVNCVNTRRPAPQOTTFPLQL-----ETGQIECTIVAKIPYDKYRIQHKYPHLPCLQVGOEKRTYLPPEVCNIVP-GQ
eIF2C 220 KVEITHCGGOMRRKRYVNCVNTRRPASHQTFPLQQ-----ESEOVECTVQYFKDRHKLYIRPHLPCLQVGOEKRTYLPPEVCNIVA-GQ
ZWILLE 372 KVEVTHRANVRKRYVAGLTPTPTRELMPVD-----EN--CTMKSVEYFOEMYGFTIQHLPCLQVGNQKASTPMEACKIVE-GQ
Sting 305 MGMVILLTDYNNKTYRIDVDVDFQSTPLCKEKTNDGEISYVDYKRYNYIIIRDLPQIMSRPTDKNIRGENDQAIMIPELARATGM-TD

RDE-1 424 RYKNEIDLVMODKFLKRAKTRKPHDYKENTLKMMLKELDFESSEELNEVERFGLCSKLQMIETCPGKVLKEPMLVNSVNEQIKMTPVIRGFOEK
F48F7.1 494 RQKGLTQVQTSYMKATARSAPEREREISNLVRKAESAD--FEAHEFGITINPAMTEVKGRVLSAPKLLYGGRTIR-ATALENQGVWDM
eIF2C 305 RCHKKLTDNOTSTMIRATARSAPDROEEISKLMRSASENTD--PYVREFGIMVQDEITDVTGRVLOPPESTLYGGRNK-AIATEVQGVWDM
ZWILLE 454 RYTRRENEKQITALKRVTCQRAEGQRNDILRTVQHNAYDQD--PYAKEFGMISEKIASVEARILPAPWLKWHENKREKQDCLFQVQGVWDM
Sting 394 AMRADFRILRAMSEHTRLNPDRIERLRMFNKRKLKCKQSV--ETLKSWNIELDSAIIVEIPARVLPPEKILFQNKQIFVCDARADWTNEF
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K ne219

FIG. 4B-1

RDE-1 514 QLNVPKEKELCCAVFVNE TAGNCPLEENDVVKFYTELIGCKFRGIRIGANENRGAQSIMYDATKNEVAFYKNCNTLNTIGRFEIAATE  
F48F7.1 581 RGKQFHTGIDIRWATACNAQOQHYNENDLRMPFVNCQRA SNDA GVPVSNPCFCCKYAVGVEQVEPMERYZKQYSG  
eIF2C 392 RNKQFHTGIDIRWATACNAQOQHYNENDLRMPFVNCQRA SNDA GVPVSNPCFCCKYAVGVEQVEPMERYZKQYSG  
ZWILLE 542 MNKKMNGMTVSRWACVNEF---RSYQENVAEGECNEIGQCEVSGEEFNPEVPIYSARPQVEKALKHVYHTSMNKT  
Sting 482 RTCSMFKNVHINRWYITPS-----RNLR--EIQEFVQGCIRTASSMKQNICNPIVEEIPDDRNGTQSOAIDNANAN-----  
RDE-1 604 AKNMFERLLPDKEQKVMFIITISKRQLNANCFVVRHYQDHTIGVANQHITSETVTALASLRHEKSGKRIFYQIALKTNAKLGGINQELDWS  
F48F7.1 658 -----KQDAWVYLRG--KRPVYAEVVRVYGDVYTGTAQOCYQAKNAIRHTP-----QTESNLCCKNNVKLGGVNSILLPN  
eIF2C 469 -----KQDAWVYLRG--KRPVYAEVVRVYGDVYTGTAQOCYQAKNAIRHTP-----QTESNLCCKNNVKLGGVNSILLPN  
ZWILLE 620 -----GKELELLALLPDNNGSLYGLKRICETELGLISQCLTKHVFISK-----QYLADVSEKINVKGGRTVVLVDA  
Sting 552 -----DPQIYVWVVRSPNEEKYSCKIKKRTCVDRPVPQVVTLKVIAPRQQ-----KPTGLMSIATKVIQMNAKLMGAP  
RDE-1 694 EIAEISPEEKERRKTMPLTMYVGIDVTHPTSYSGIDYSIAAWVASINPGGT-IYRNMIVTQEECRPGERAVAHGRE---RTDILEAKFVK  
F48F7.1 725 V-----ERRIENEPIVITGGDITHPFAGDSRKPISIAAWVSDAHPB-RYKATVRVQOHRQETISDITY-----MVRE  
eIF2C 536 G-----RPPVEQQPVITELGVDVTHPAGDCKUPISIAAWVSDAHPN-RYKATVRVQOHRQETISDITY-----MVRE  
ZWILLE 691 IS-----CRIFLYSDIPTIIFGPDVTHPENGEESSEPSIAAWVASODWPEVTKYAGLVCQAHRQELIQDHYKTWQDPVRGTVSGGMIRD  
Sting 621 W-----QVVIPLHGLMTVGEDVCHSP--KNKNKSYGAFAVATMDQKESFYFSTYNEHIKGOELSEQMSVN-----MAC

FIG. 4B-2

\* ne300

RDE-1	780	LLREFAENNDNRAPAHITVYRDGVSDSEMLRVSHDELRSIKSEVKQFMSESDGEDPEPKYTFIVLOKRHNTRLLRRMEKDKPVPVNKQLTP
F48F7.1	792	LLVQEFYRNTR-FKPARIVYRDGVSGQTFNVQVELRAITREACMMTERGYQPG-----ITFIAVOKRHHTRLEAVDKDO--V
eIF2C	603	LLIGEFYKSTR-FKPTRATVYRDGVSGQTFQVHHEILLIRENCIKLEKDYQPG-----ITFIVOKRHHTRLECTEKNER--V
ZWILLE	775	LLISERKATG-QKPLRIHIVYRDGVSGQFYQVMEIYELDAYRKACASLEPNIQPP-----VTFIVOKRHHTRLEANNHRDKNST
Sting	687	ALRSYQEQHR-SLPERIIEFRDGVGDQLYQVNVSEVNTDKDLDEIYSAGKQEGC-RMTFIIYSKRINSRLETGHRNPV-----
RDE-1	870	AETDVAAVAKQWEEDMKESKETGIVNPSSGTTVDKILVSKYKEDFEELASHHGVLGTSRPGHYTVMYDDKGMQDEVIKMTYGLAFLSAR
F48F7.1	868	-----GKAYNTPFGTTVDVGIHTPTTEDEFLCSHAGTCTSRPSHYHVRVDDNNHTADELQQLTYQMCHTYIR
eIF2C	679	-----GKGNTPAGTTVDINKTHTTEDEFLCSHAGTCTSRPSHYHVRVDDNNHTADELQQLTYQMCHTYIR
ZWILLE	853	-----DRSGNILEGTTVDENKICHTTEDEFLCSHAGTCTSRPAHYHVRDENNTDGIQSTENNLCYTYAR
Sting	766	-----F-GTVVDDVITLEERYDDEFLVQA VRI GTVSTSVNVISDNNNGENADKLOMISYKMTHTMFIN
RDE-1	960	CRKPISLPVEVHYAHLSCCKKELRYRKYEHYICDYAOPRTRHEMEFIFLOTNVKYPGMSEA----- (SEQ ID NO: 13)
F48F7.1	936	CTRSVSTPAPAYAHLYAHFARVHLVDBREHDSGEGSOPSGCSSEDTILSNMRAVQVILANLVS----- (SEQ ID NO: 9)
eIF2C	747	CTRSVSTPAPAYAHLYAHFARVHLVDBREHDSAGSHTSGQSNGRDQALAAVAVQHODTLRMYFA----- (SEQ ID NO: 10)
ZWILLE	921	CTRSVSTVPPAYAHILAAAFARFYLEPEIMQDNCSFGKKNKTKTTVGDVGVRPLPALKENVKRVMEYC----- (SEQ ID NO: 6)
Sting	827	YSGTIRVPVAVCHYAHKLAFLVAESINRAPSAGLQNLXFL----- (SEQ ID NO: 7)

FIG. 4B-3

cagccacaagtgatgaacatgtctcgaatttcccgaaattggaaaaaggattttatcgtcattctctcgatccggta  
tgatcaattattagcagctataagataataaagtgttgataattatattatagggagatgaaatggcctgcgagggcccactg  
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ataataataataatcaccicaactatttatattttaagacaattcgcgaaaaattttgtgtacgataataatcaat

FIG. 5A



tctgcgagttcctgaatcgtttcacgateccaaacagattcgaacaatcattagaagtagcaccaagaatcgaagcatggt  
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ggagcaaaagaatacgtgtaccaatggaacatcttgaagttcatgagaagccacaaagatacaagaatcgaattgatc  
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ggaaaggttttgaaagagccaatgcttgtgaatagtgtaaatgaacaaattaaaatgacaccagtgattcgtggatttca  
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gcttagaagagaacgacgttgtgaagtgtttctacgtagattattccgaaatattttcagtaagttctacacgaaact  
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ttcgtgaaattgctcagagaattcgcagaagtgagttgtcttgagtatttaaaagatctctgggatttttaattttttg

FIG. 5B

taaaactttcagaaacaacgacaaatcgagcaccacgcatatattgtatgtctatcggagacggaggttagcgcgattcgggagatgctata  
cgtgttagtcatagtatgagcttcgatcttttaaaaaagcgaaagttaaaaaacaattcatgtcgggaacggggaatgggagaaagatcccaag  
ggccgaaagtacacgttcatgtgtattcagaaaaagacacatacacagattgcttcggaaagaaatggaaaaaagataaagcccaatgg  
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aaaaagaaactggaaattgtgaaccccatcatcccggaacaaactgtgggataaaaacttatcgttttcgaaatacaaaaattcgaatttttt  
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aatgtttcagaaaatgacctacggacttgcctttctctctgtctatgtatgtcgaaaaacccatctcgttgccttgccttcgggttc  
attatgtctatttatcatgtgaaaaagcgaaagaggttttatcgaacttacaaaggaaacattacatcgtgtgactatgcacag  
ccacgggactcgacagaaaatgggaacattttctccaaaactaacgtgaaagtaccttgggaatgtcgttcgcataaacatttttgc  
aaaaagtgtgcgccgttcaatcaaattttcaattgtagatattgtactactattttttaagcccggtttcaaaaatt  
cattccatgactaacgttttcataaaattacttgaattt (SEQ ID NO:1)

Title: RNA INTERFERENCE PATHWAY GENES AS TOOLS  
FOR TARGETED GENETIC INTERFERENCE

CAGCCACAAAGTGATGAAAC- 3' UTR

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1/1                               31/11
ATG TCC TCG AAT TTT CCC GAA TTG GAA AAA GGA TTT TAT CGT CAT TCT CTC GAT CCG GAG
Met ser ser asn pro pro glu leu glu lys gly phe tyr arg his ser leu asp pro glu

61/21                               91/31
ATG AAA TGG CTT GCG AGG CCC ACT GGT AAA TGC GAC GGC AAA TTC TAT GAG AAG AAA GTA
met lys trp leu ala arg pro thr gly lys cys asp gly lys phe tyr glu lys lys val

121/41                              151/51
CTT CTT TTG GTA AAT TGG TTC AAG TTC TCC AGC AAA ATT TAC GAT CGG GAA TAC TAC GAG
leu leu leu val asn trp phe lys phe ser ser lys ile tyr asp arg glu tyr tyr glu

181/61                              211/71
TAT GAA GTG AAA ATG ACA AAG GAA GTA TTG AAT AGA AAA CCA GGA AAA CCT TTC CCA AAA
tyr glu val lys met thr lys glu val leu asn arg lys pro gly lys pro phe pro lys

241/81                              271/91
AAG ACA GAA ATT CCA ATT CCC GAT CGT GCA AAA CTC TTC TGG CAA CAT CTT CGG CAT GAG
lys thr glu ile pro ile pro asp arg ala lys leu phe trp gln his leu arg his glu

301/101                             331/111
AAG AAG CAG ACA GAT TTT ATT CTC GAA GAC TAT GTT TTT GAT GAA AAG GAC ACT GTT TAT
lys lys gln thr asp phe ile leu glu asp tyr val phe asp glu lys asp thr val tyr

361/121                             391/131
AGT GTT TGT CGA CTG AAC ACT GTC ACA TCA AAA ATG CTG GTT TCG GAG AAA GTA GTA AAA
ser val cys arg leu asn thr val thr ser lys met leu val ser glu lys val val lys

421/141                             451/151
AAG GAT TCG GAG AAA AAA GAT GAA AAG GAT TTG GAG AAA AAA ATC TTA TAC ACA ATG ATA
lys asp ser glu lys lys asp glu lys asp leu glu lys lys ile leu tyr thr met ile

481/161                             511/171
CTT ACC TAT CGT AAA AAA TTT CAC CTG AAC TTT AGT CGA GAA AAT CCG GAA AAA GAC GAA
leu thr tyr arg lys lys phe his leu asn phe ser arg glu asn pro glu lys asp glu

541/181                             571/191
GAA GCG AAT CGG AGT TAC AAA TTC CTG AAG AAT GTT ATG ACC CAG AAA GTT CGC TAC GCG
glu ala asn arg ser tyr lys phe leu lys asn val met thr gln lys val arg tyr ala

601/201                             631/211
CCT TTT GTG AAC GAG GAG ATT AAA GTA CAA TTC GCG AAA AAT TTT GTG TAC GAT AAT AAT
pro phe val asn glu glu ile lys val gln phe ala lys asn phe val tyr asp asn asn

661/221                             691/231
TCA ATT CTG CGA GTT CCT GAA TCG TTT CAC GAT CCA AAC AGA TTC GAA CAA TCA TTA GAA
ser ile leu arg val pro glu ser phe his asp pro asn arg phe glu gln ser leu glu

721/241                             751/251
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FIG. 6A

GTA GCA CCA AGA ATC GAA GCA TGG TTT GGA ATT TAC ATT GGA ATC AAA GAA TTG TTC GAT  
 val ala pro arg ile glu ala trp phe gly ile tyr ile gly ile lys glu leu phe asp  
 731/261 811/271  
 GGT GAA CCT GTG CTC AAT TTT GCA ATT GTC GAT AAA CTA TTC TAC AAT GCA CCG AAA ATG  
 gly glu pro val leu asn phe ala ile val asp lys leu phe tyr asn ala pro lys met  
 841/281 871/291  
 TCT CTT CTG GAT TAT CTT CTC CTA ATT GTC GAC CCC CAG TCG TGT AAC GAT GAT GTA CGA  
 ser leu leu asp tyr leu leu leu ile val asp pro gln ser cys asn asp asp val arg  
 901/301 931/311  
 AAA GAT CTT AAA ACA AAA CTG ATG GCG GGA AAA ATG ACA ATC AGA CAA GCC GCG CGG CCA  
 lys asp leu lys thr lys leu met ala gly lys met thr ile arg gln ala ala arg pro  
 961/321 991/331  
 AGA ATT CGA CAA TTA TTG GAA AAT TTG AAG CTG AAA TGC GCA GAA GTT TGG GAT AAC GAA  
 arg ile arg gln leu leu glu asn leu lys leu lys cys ala glu val trp asp asn glu  
 1021/341 1051/351  
 ATG TCG AGA TTG ACA GAA CGA CAT CTG ACA TTT CTA GAT TTG TGC GAG GAA AAC TCT CTT  
 met ser arg leu thr glu arg his leu thr phe leu asp leu cys glu glu asn ser leu  
 1081/361 1111/371  
 GTT TAT AAA GTC ACT GGT AAA TCG GAC AGA GGA AGA AAT GCA AAA AAG TAC GAT ACT ACA  
 val tyr lys val thr gly lys ser asp arg gly arg asn ala lys lys<sup>4</sup> tyr asp thr thr  
 1141/381 1171/391  
 TTG TTC AAA ATC TAT GAG GAA AAC AAA AAG TTC ATT GAG TTT CCC CAC CTA CCA CTA GTC  
 leu phe lys ile tyr glu glu asn lys lys phe ile glu phe pro his leu pro leu val  
 1201/401 1231/411  
 AAA GTT AAA AGT GGA GCA AAA GAA TAC GCT GTA CCA ATG GAA CAT CTT GAA GTT CAT GAG  
 lys val lys ser gly ala lys glu tyr ala val pro met glu his leu glu val his glu  
 1261/421 1291/431  
 AAG CCA CAA AGA TAC AAG AAT CGA ATT GAT CTG GTG ATG CAA GAC AAG TTT CTA AAG CGA  
 lys pro gln arg tyr lys asn arg ile asp leu val met gln asp lys phe leu lys arg  
 1321/441 1351/451  
 GCT ACA CGA AAA CCT CAC GAC TAC AAA GAA AAT ACC CTA AAA ATG CTG AAA GAA TTG GAT  
 ala thr arg lys pro his asp tyr lys glu asn thr leu lys met leu lys glu leu asp  
 1381/461 1411/471  
 TTC TCT TCT GAA GAG CTA AAT TTT GTT GAA AGA TTT GGA TTA TGC TCC AAA CTT CAG ATG  
 phe ser ser glu glu leu asn phe val glu arg phe gly leu cys ser lys leu gln met  
 1441/481 1471/491  
 ATC GAA TGT CCA GGA AAG GTT TTG AAA GAG CCA ATG CTT GTG AAT AGT GTA AAT GAA CAA  
 ile glu cys pro gly lys val leu lys glu pro met leu val asn ser val asn glu gln  
 1501/501 1531/511  
 ATT AAA ATG ACA CCA GTG ATT CGT GGA TTT CAA GAA AAA CAA TTG AAT GTG GTT CCC GAA  
 ile lys met thr pro val ile arg gly phe gln glu lys gln leu asn val val pro glu

FIG. 6B

1561/521	1591/531
AAA GAA GTT TGC TGT GGT GTT TTT GTA GTC AAC GAA ACA GCG GGA AAT CCA TGC TTA GAA	
lys glu leu cys cys ala val phe val val asn glu thr ala gly asn pro cys leu glu	
1621/541	1651/551
GAG AAC GAC GTT GTT AAG TTC TAC ACC GAA CTA ATT GGT GGT TGC AAG TTC CGT GGA ATA	
glu asn asp val val lys phe tyr thr glu leu ile gly gly cys lys phe arg gly ile	
1681/561	1711/571
CGA ATT GGT GCC AAT GAA AAC AGA GGA GCG CAA TCT ATT ATG TAC GAC GCG ACG AAA AAT	
arg ile gly ala asn glu asn arg gly ala gln ser ile met tyr asp ala thr lys asn	
1741/581	1771/591
GAA TAT GCC TTC TAC AAA AAT TGT ACA CTA AAT ACC GGA ATC GGT AGA TTT GAA ATA GCC	
glu tyr ala phe tyr lys asn cys thr leu asn thr gly ile gly arg phe glu ile ala	
1901/601	1831/611
GCA ACA GAA GCG AAG AAT ATG TTT GAA CGT CTT CCC GAT AAA GAA CAA AAA GTC TTA ATG	
ala thr glu ala lys asn met phe glu arg leu pro asp lys glu gln lys val leu met	
1861/621	1891/631
ITC ATT ATC ATT TCC AAA CGA CAA CTG AAT GCT TAC GGT TTT GTG AAA CAT TAT TGC GAT	
phe ile ile ile ser lys arg gln leu asn ala tyr gly phe val lys his tyr cys asp	
1921/641	1951/651
CAC ACC ATC GGT GTA GCT AAT CAG CAT ATT ACT TCT GAA ACA GTC ACA AAA GCT TTG GCA	
his thr ile gly val ala asn gln his ile thr ser glu thr val thr lys ala leu ala	
1981/661	2011/671
TCA CTA AGG CAC GAG AAA GGA TCA AAA CGA ATT TTC TAT CAA ATT GCA TTG AAA ATC AAC	
ser leu arg his glu lys gly ser lys arg ile phe tyr gln ile ala leu lys ile asn	
2041/681	2071/691
GCG AAA TTA GGA GGT ATT AAC CAG GAG CTT GAC TGG TCA GAA ATT GCA GAA ATA TCA CCA	
ala lys leu gly gly ile asn gln glu leu asp trp ser glu ile ala glu ile ser pro	
2101/701	2131/711
GAA GAA AAA GAA AGA CCG AAA ACA ATG CCA TTA ACT ATG TAT GTT GGA ATT GAT GTA ACT	
glu glu lys glu arg arg lys thr met pro leu thr met tyr val gly ile asp val thr	
2161/721	2191/731
CAT CCA ACC TCC TAC AGT GGA ATT GAT TAT TCT ATA GCG GCT GTA GTA GCG AGT ATC AAT	
his pro thr ser tyr ser gly ile asp tyr ser ile ala ala val val ala ser ile asn	
2221/741	2251/751
CCA GGT GGA ACT ATC TAT CGA AAT ATG ATT GTG ACT CAA GAA GAA TGT CGT CCC GGT GAG	
pro gly gly thr ile tyr arg asn met ile val thr gln glu glu cys arg pro gly glu	
2281/761	2311/771
CGT GCA GTG GCT CAT GGA CCG GAA AGA ACA GAT ATT TTG GAA GCA AAG TTC GTG AAA TTG	
arg ala val ala his gly arg glu arg thr asp ile leu glu ala lys phe val lys leu	
2341/781	2371/791
ATC AGA GAA TTC GCA GAA AAC AAC GAC AAT CGA GCA CCA GCG CAT ATT GTA GTC TAT CGA	
leu arg glu phe ala glu asn asn asp asn arg ala pro ala his ile val val tyr arg	

FIG. 6C

Title: RNA INTERFERENCE PATHWAY GENES AS TOOLS  
FOR TARGETED GENETIC INTERFERENCE

2401/801  
GAC GGA GTT AGC GAT TCG GAG ATG CTA CGT GTT AGT CAT GAT GAG CTT CGA TCT TTA AAA  
asp gly val ser asp ser glu met leu arg val ser his asp glu leu arg ser leu lys

2461/821  
AGC GAA GTA AAA CAA TTC ATG TCG GAA CGG GAT GGA GAA GAT CCA GAG CCG AAG TAC ACG  
ser glu val lys gln phe met ser glu arg asp gly glu asp pro glu pro lys tyr thr

2521/841  
TTC ATT GTG ATT CAG AAA AGA CAC AAT ACA CGA TTG CTT CGA AGA ATG GAA AAA GAT AAG  
phe ile val ile gln lys arg his asn thr arg leu leu arg arg met glu lys asp lys

2581/861  
CCA GTG GTC AAT AAA GAT CTT ACT CCT GCT GAA ACA GAT GTC GCT GTT GCT GCT GTT AAA  
pro val val asn lys asp leu thr pro ala glu thr asp val ala val ala ala val lys

2641/881  
CAA TGG GAG GAG GAT ATG AAA GAA AGC AAA GAA ACT GGA ATT GTG AAC CCA TCA TCC GGA  
gln trp glu glu asp met lys glu ser lys glu thr gly ile val asn pro ser ser gly

2701/901  
ACA ACT GTG GAT AAA CTT ATC GTT TCG AAA TAC AAA TTC GAT TTT TTC TTG GCA TCT CAT  
thr thr val asp lys leu ile val ser lys tyr lys phe asp phe phe leu ala ser his

2761/921  
CAT GGT GTC CTT GGT ACA TCT CGT CCA GGA CAT TAC ACT GTT ATG TAT GAC GAT AAA GGA  
his gly val leu gly thr ser arg pro gly his tyr thr val met tyr asp asp lys gly

2821/941  
ATG AGC CAA GAT GAA GTC TAT AAA ATG ACC TAC GGA CTT GCT TTT CTC TCT GCT AGA TGT  
met ser gln asp glu val tyr lys met thr tyr gly leu ala phe leu ser ala arg cys

2881/961  
CGA AAA CCC ATC TCG TTG CCT GTT CCG GTT CAT TAT GCT CAT TTA TCA TGT GAA AAA GCG  
arg lys pro ile ser leu pro val pro val his tyr ala his leu ser cys glu lys ala

2941/981  
AAA GAG CTT TAT CGA ACT TAC AAG GAA CAT TAC ATC GGT GAC TAT GCA CAG CCA CGG ACT  
lys glu leu tyr arg thr tyr lys glu his tyr ile gly asp tyr ala gln pro arg thr

3001/1001  
CGA CAC GAA ATG GAA CAT TTT CTC CAA ACT AAC GTG AAG TAC CCT GGA ATG TCG TTC GCA  
arg his glu met glu his phe leu gln thr asn val lys tyr pro gly met ser phe ala

3061/1021  
TAA CAT TTT GCA AAA GTG TCG CCC GTT TCA ATC AAA TTT TTC AAT TGT AGA TAT TGT ACT  
OCH (SEQ ID NO:3)

3121/1041  
TAC TTT TTT TTA AAG CCC GGT TTC AAA AAT TCA TTC CAT GAC TAA CGT TTT CAT AAA TTA

3191/1061  
CTT GAA ATT TAA AAA AAA AAA AAA AAA (SEQ ID NO:2)

FIG. 6D

Title: RNA INTERFERENCE PATHWAY GENES AS TOOLS  
 FOR TARGETED GENETIC INTERFERENCE

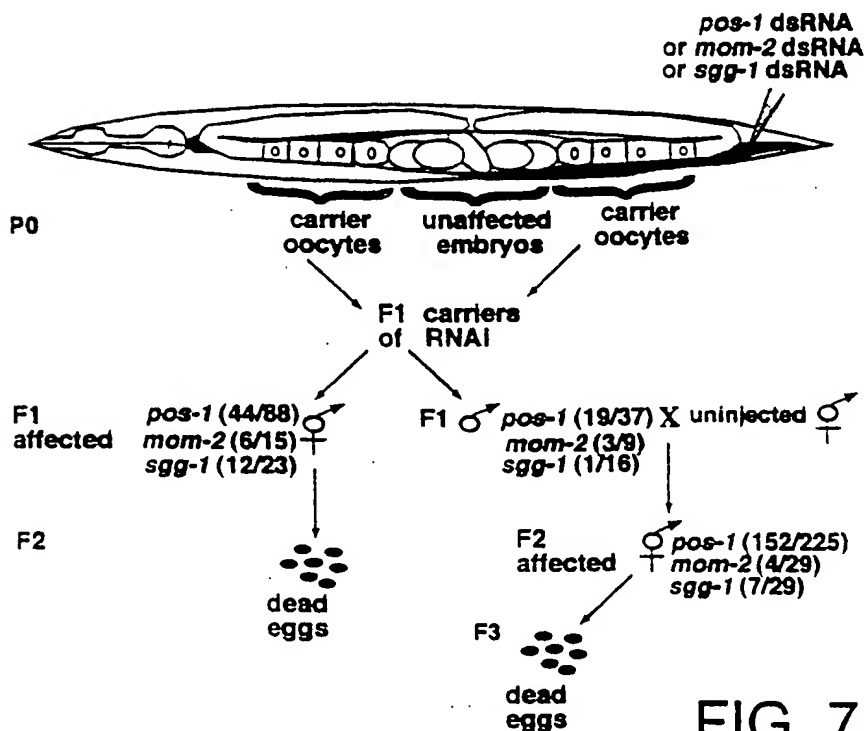
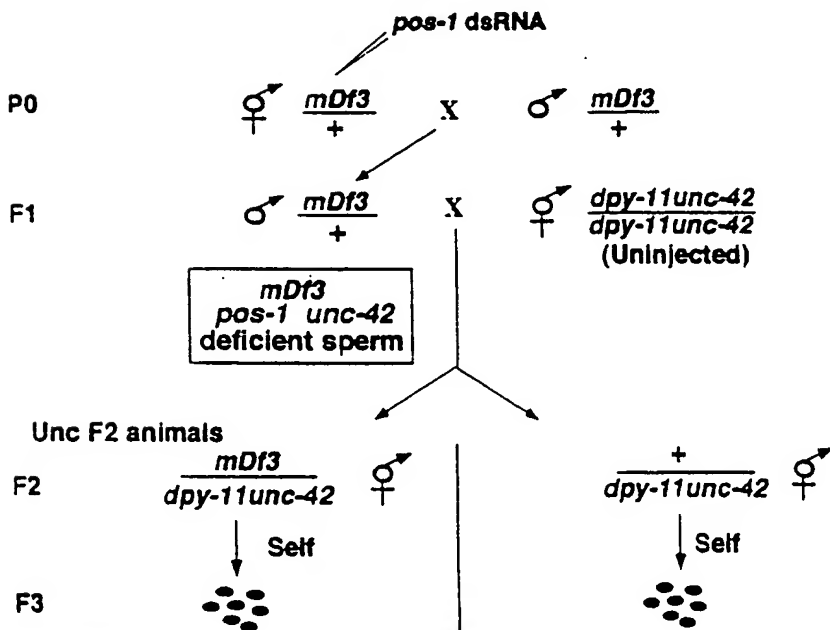


FIG. 7A



Results:

6/9 *mDf3* sperm gave rise to F2 with 100% ( $n > 1000$ ) F3 *pos-1* embryos.

3/27 (+) sperm gave rise to F2 with 100% ( $n > 500$ ) F3 *pos-1* embryos.

FIG. 7B





Injected P0	F1
 $\frac{\text{pos-1 dsRNA} \text{ } rde-1 \text{ } unc-42}{+}$ self X	$rde-1 (-)$ 11/24 $rde-1 (+)$ 9/72
 $\frac{rde-2 \text{ } unc-13}{+}$ →	$rde-2 (-)$ 0/39 $rde-2 (+)$ 23/78
 $\frac{mut-7 \text{ } dpy-17}{+}$ →	$mut-7 (-)$ 0/15 $mut-7 (+)$ 20/50
 $\frac{rde-4 \text{ } unc-69}{+}$ →	$rde-4 (-)$ 5/15 $rde-4 (+)$ 11/48

FIG. 8A



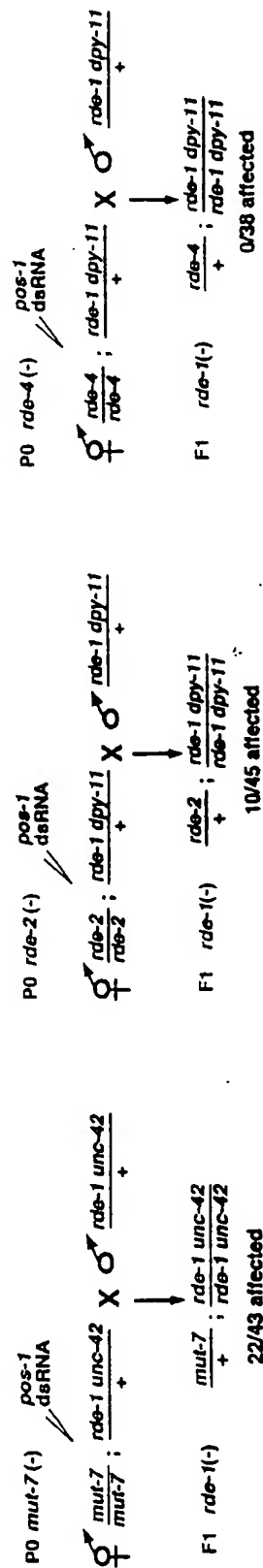
P0	Injected F1
 $\frac{rde-1 \text{ } unc-42}{+}$ →	$\frac{\text{pos-1 dsRNA} \text{ } rde-1 \text{ } unc-42}{rde-1 \text{ } unc-42}$ 0/37
 $\frac{rde-4 \text{ } unc-69}{+}$ →	$\frac{rde-4 \text{ } unc-69}{rde-4 \text{ } unc-69}$ 0/37

FIG. 8B





**FIG. 9B**

10 20 30 40 50 60  
ATGGATTTTAACCCTAAGTTTGAAGCGTTTTTCGGTGGATCAGATGTTCTATGAAG  
M D L T K L T F E S V F G G S D V P M K

70 80 90 100 110 120  
CCTTCCCCTCGGAGGATAACAAAACGCCAAGAAACAGAACAGATTTGGAGATGTTTCTG  
P S R S E D N K T P R N R T D L E M F L

130 140 150 160 170 180  
AAGAACTCCCTCATGGTACTAGAAGAGGCTGCTAAGGCTGTCTATCAAAAGACGCCA  
K K T P L M V L E E A A K A V Y Q K T P

190 200 210 220 230 240  
ACTTGGGGCACTGTGCAACTTCCTGAAGGCTTCGAGATGACGTTGATTCTGAATGAAATT  
T W G T V E L P E G F E M T L I L N E I

250 260 270 280 290 300  
ACTGTAAAAGGCCAGGCAACAAGCAAGAAAGCTGCGAGACAAAAGGCTGCTGTTGAATAT  
T V K G Q A T S K K A A R Q K A A V E Y

310 320 330 340 350 360  
TTACGCAAGGTTGTGGAGAAAGGAAAGCACGAAATCTTTTTCATTCTGGAACAACCAAA  
L R K V V E K G K H E I F F I P G T T K

370 380 390 400 410 420  
GAAGAAGCTCTTTTGAATATTGATCAAAATATCGGATAAGGCTGAGGAATTGAAACGATCA  
E E A L S N I D Q I S D K A E E L K R S

430 440 450 460 470 480  
ACTTCAGATGCTGTTTCAGGATAACGATAACGATGATTTCGATTCTACAAGTGCTGAATTT  
T S D A V Q D N D N D D S I P T S A E F

490 500 510 520 530 540  
CCACCTGGTATTTTCGCCAACCGAGAATTGGGTGCGAAAGTTGCAGGAAAAATCTCAAAAA  
P P G I S P T E N W V G K L Q E K S Q K

550 560 570 580 590 600  
AGCAAGCTGCAAGCCCCAATCTATGAAGATTCCAAGAATGAGAGAACCGAGCGTTTCTTG  
S K L Q A P I Y E D S K N E R T E R F L

610 620 630 640 650 660  
GTTATATGCACGATGTGCAATCAAAAAACCGAGGAATCAGAAGTAAGAAGAAGGACGCA  
V I C T M C N Q K T R G I R S K K K D A

670 680 690 700 710 720  
AAGAATCTTGCAGCATGGTTGATGTGGAAGCGTTGGAAGACGGTATCGAATCTCTGGAA  
K N L A A W L M W K A L E D G I E S L E

730 740 750 760 770 780  
TCATATGATATGGTTGATGTGATTGAAAATTTGGAAGAAGCTGAACATTTACTCGAAATT  
S Y D M V D V I E N L E E A E H L L E I

FIG. 10A

```

      790      800      810      820      830      840
CAGGATCAAGCATCCAAGATTAAAGACAAGCATTCCGCACTGATTGATATACTCTCGGAC
Q D Q A S K I K D K H S A L I D I L S D

      850      860      870      880      890      900
AAGAAAAGATTTTTCAGACTACAGCATGGATTTCAACGTATTATCAGTGAGCACAATGGGA
K K R F S D Y S M D F N V L S V S T M G

      910      920      930      940      950      960
ATACATCAGGTGCTATTGGAAATCTCGTTCCGGCGTCTAGTTTCTCCAGACCCCGACGAT
I H Q V L L E I S F R R L V S P D P D D

      970      980      990      1000      1010      1020
TTGGAAATGGGAGCAGAACACACCCAGACTGAAGAAATTATGAAGGCTACTGCCGAGAAG
L E M G A E H T Q T E E I M K A T A E K

      1030      1040      1050      1060      1070      1080
GAAAAGCTACGGAAGAAGAATATGCCAGATTCCGGGCCGCTAGTGTTTGCTGGACATGGT
E K L R K K N M P D S G P L V F A G H G

      1090      1100      1110      1120      1130      1140
TCATCGGCGGAAGAGGCTAAACAGTGTGCTTGTAATCGGCGATTATCCATTTCAACACC
S S A E E A K Q C A C K S A I I H F N T

      1150      1160      1170      1180      1190      1200
TATGATTTTCACGGATTGAAAATATTATTGCGTATTCCTGAAAAATGAAGCGTCTGAATGA
Y D F T D * K Y Y C V F L K N E A S E *

      1210      1220      1230
TTATAAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:4)
L * K K K K K (SEQ ID NO:5)

```

FIG. 10B

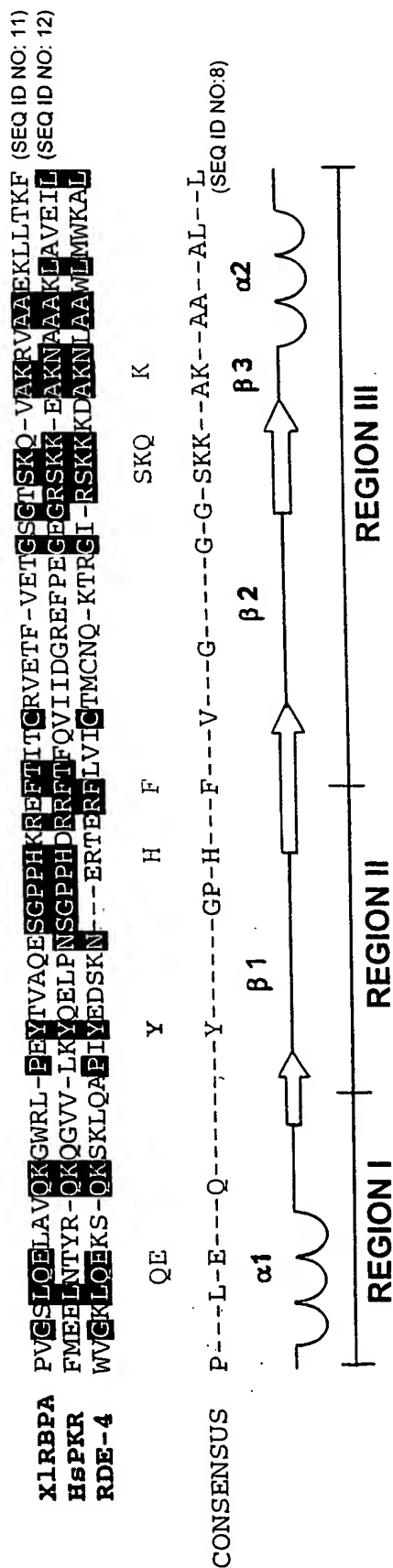
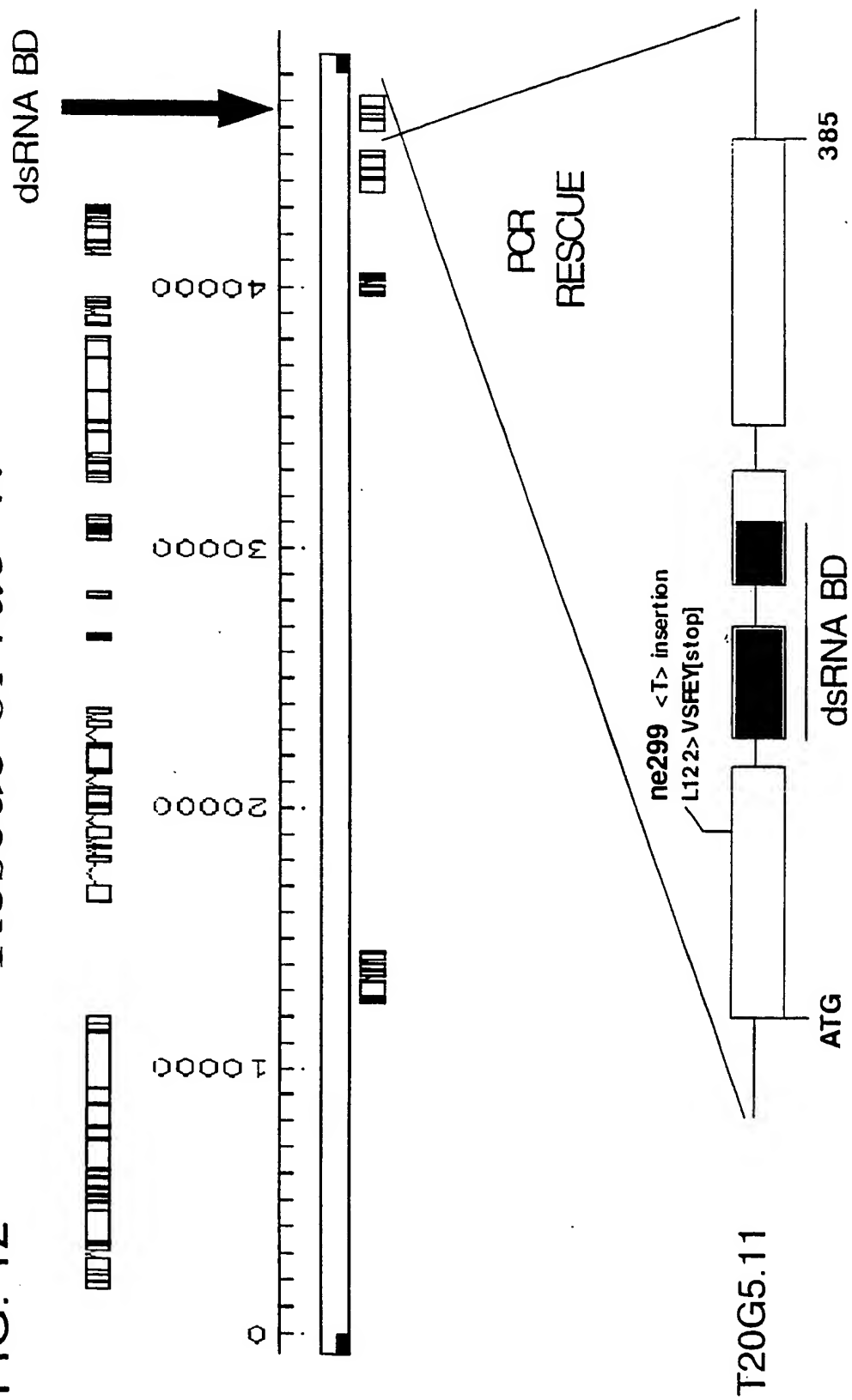


FIG. 11

Rescue of *rde-4*:

FIG. 12



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